This listing of claims will replace all prior versions, and listings, of claims in the application.

Listing of Claims:

1. (Currently amended) A method for making a hypermutable bacterium comprising the steps of:

introducing into a bacterium a polynucleotide encoding a dominant negative PMS2 mismatch repair protein under the control of an inducible transcription regulatory sequence; and

inducing said inducible transcription regulatory sequence in said bacterium;

wherein said polynucleotide comprises a truncation mutation, wherein said dominant negative PMS2 mismatch repair protein is a truncated protein, and wherein said dominant negative PMS2 mismatch repair protein exerts a dominant negative effect on mismatch repair when expressed in said bacterium, whereby said bacterium becomes hypermutable.

2-5. (Canceled)

6. (Previously presented) The method of claim 1 wherein the dominant negative PMS2 mismatch repair protein is a dominant negative human PMS2 protein.

7. (Previously presented) The method of claim 1 wherein the dominant negative mismatch repair protein is a dominant negative plant PMS2 protein.

8-15. (Canceled)

16. (Previously presented) The method of claim 7 wherein said polynucleotide encoding a dominant negative PMS2 mismatch repair protein comprises a truncation mutation at codon 134.

17. (Previously presented) The method of claim 6 wherein said polynucleotide encoding a dominant negative PMS2 mismatch repair protein comprises a truncation mutation at codon 134.

18. (Currently amended) A homogeneous composition of induced, cultured, hypermutable bacteria which comprise a polynucleotide encoding a dominant negative mismatch repair

protein under the control of an inducible transcription regulatory sequence, wherein said polynucleotide comprises a truncation mutation, and wherein said dominant negative mismatch repair protein is a truncated dominant negative PMS2 mismatch repair protein, wherein said truncated dominant negative PMS2 mismatch repair protein exerts a dominant negative effect when expressed in said bacteria.

19-25. (Canceled)

26. (Previously presented) The homogeneous composition of claim 18 wherein the bacteria express a protein which consists of the first 133 amino acids of PMS2.

27. (Previously presented) The homogeneous composition of claim 26 wherein the dominant negative PMS2 mismatch repair protein is a dominant negative human PMS2 mismatch repair protein.

28-70. (Canceled)

71. (Previously presented) The method of claim 1 wherein the polynucleotide encoding a dominant negative PMS2 mismatch repair protein comprises a truncation mutation at codon 134.

72. (Previously presented) A method for making a hypermutable bacterium comprising the steps of:

introducing into a bacterium a polynucleotide encoding a dominant negative mismatch repair protein under the control of an inducible transcription regulatory sequence, wherein said dominant negative mismatch repair protein is selected from the group consisting of a dominant negative PMSR and a dominant negative PMS2L mismatch repair protein; and

inducing said bacterium;

wherein said dominant negative mismatch repair protein exerts a dominant negative effect on mismatch repair when expressed in said bacterium, whereby said bacterium becomes hypermutable.

73. (Previously presented) A homogeneous composition of induced, cultured, hypermutable bacteria which comprise a polynucleotide encoding a dominant negative mismatch repair protein selected from the group consisting of a dominant negative PMSR and a dominant negative PMS2L mismatch repair protein under the control of an inducible transcription regulatory sequence, wherein said dominant negative mismatch repair protein exerts a dominant negative effect when expressed in said bacteria.

74. (New) The composition of claim 26 wherein the PMS2 mismatch repair protein is a plant PMS2 mismatch repair protein.

75. (New) The composition of 74 wherein the plant PMS2 mismatch repair protein is an *Arabidopsis thaliana* PMS2 mismatch repair protein.

76. (New) The method of claim 7 wherein the dominant negative PMS2 protein is an *Arabidopsis thaliana* PMS2 protein.

77. (New) The method of claim 16 wherein the dominant negative PMS2 protein is an *Arabidopsis thaliana* PMS2 protein.

78. (New) The homogeneous composition of claim 26 wherein the dominant negative PMS2 mismatch repair protein is a dominant negative *Arabidopsis thaliana* PMS2 mismatch repair protein.